STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/589,955_

Source: _IFWP_

Date Processed by STIC: _8/28/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
       http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
    U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/589,955_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length

The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4__✓__Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length

Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences (OLD RULES)

Sequence(s)_____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences (NEW RULES)

Sequence(s)_____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n or Xaa**, and which residue **n or Xaa** represents.

10____Invalid <213> Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11____Use of <220>

Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12____PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n/Xaa

"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

IFWp

RAW SEQUENCE LISTING   DATE: 08/28/2006
PATENT APPLICATION: US/10/589,955   TIME: 09:40:09

        Input Set : A:\PTO.RJ.txt
        Output Set: N:\CRF4\08282006\J589955.raw

    3 <110> APPLICANT: National Institute of Advanced Industrial Science and Technology
    4   Kinki University
    5   Kitakyushu Foundation for the Advancement of Industry   *see item 4 on*
    7 <120> TITLE OF INVENTION: Cytoplasm-localized DNA and RNA
    9 <130> FILE REFERENCE: 05-102NIQ   *Error Summary*
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/589,955   *Sheet*
C--> 11 <141> CURRENT FILING DATE: 2006-08-18
   11 <150> PRIOR APPLICATION NUMBER: JP 2004-045488
   12 <151> PRIOR FILING DATE: 2004-02-20   *Does Not Comply*
   14 <150> PRIOR APPLICATION NUMBER: JP 2004-136228   *Corrected Diskette Needed*
   15 <151> PRIOR FILING DATE: 2004-04-30
   17 <160> NUMBER OF SEQ ID NOS: 28   *see pp 1-6*
   19 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

    133 <210> SEQ ID NO: 9
    134 <211> LENGTH: 21
    135 <212> TYPE: RNA
    136 <213> ORGANISM: Artificial
    138 <220> FEATURE:
    139 <223> OTHER INFORMATION: Probe   *t's not allowed in an RNA sequence.*
    141 <400> SEQUENCE: 9   *For a combined DNA/RNA sequence,*
E--> 142 cuacaucacg ccagucaact t   *use <212> DNA and explain in*
    145 <210> SEQ ID NO: 10   *<220>-<223>*
    146 <211> LENGTH: 21   21   *section*
    147 <212> TYPE: RNA
    148 <213> ORGANISM: Artificial
    150 <220> FEATURE:
    151 <223> OTHER INFORMATION: Probe   *same error*
    153 <400> SEQUENCE: 10
E--> 154 guugacuggc gugauguac t   21
    259 <210> SEQ ID NO: 19
    260 <211> LENGTH: 22   *same*
    261 <212> TYPE: RNA
    262 <213> ORGANISM: Artificial
    264 <220> FEATURE:
    265 <223> OTHER INFORMATION: Linker
    267 <220> FEATURE:
    268 <221> NAME/KEY: modified_base
    269 <222> LOCATION: (1)..(1)
    270 <223> OTHER INFORMATION: Linker

RAW SEQUENCE LISTING   DATE: 08/28/2006
PATENT APPLICATION: US/10/589,955   TIME: 09:40:09

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\08282006\J589955.raw

"n" can only represent a single nucleotide, nothing else

```
273 <220> FEATURE:
274 <221> NAME/KEY: misc_feature
275 <222> LOCATION: (1)..(1)
276 <223> OTHER INFORMATION: "n" is -O-CH.sub.2CH.sub.2-O-CH.sub.2CH.sub.2-NH.sub.2
279 <400> SEQUENCE: 19
```
E--> 280 ncuacaucac gccagucaac tt   22
```
283 <210> SEQ ID NO: 20
284 <211> LENGTH: 22
285 <212> TYPE: RNA
286 <213> ORGANISM: Artificial
288 <220> FEATURE:
289 <223> OTHER INFORMATION: Linker
291 <220> FEATURE:
292 <221> NAME/KEY: modified_base
293 <222> LOCATION: (1)..(1)
294 <223> OTHER INFORMATION: Linker
297 <220> FEATURE:
298 <221> NAME/KEY: misc_feature
299 <222> LOCATION: (1)..(1)
```

same error as above

```
300 <223> OTHER INFORMATION: "n" is -O-CH.sub.2CH.sub.2-O-CH.sub.2CH.sub.2-NH.sub.2
303 <400> SEQUENCE: 20
```
E--> 304 nguugacugg cgugauguag tt   22
```
307 <210> SEQ ID NO: 21
308 <211> LENGTH: 21
309 <212> TYPE: RNA
310 <213> ORGANISM: Artificial
312 <220> FEATURE:
```

this does not describe Artificial Sequence

```
313 <223> OTHER INFORMATION: Modified thymidine
315 <220> FEATURE:
316 <221> NAME/KEY: modified_base
317 <222> LOCATION: (20)..(20)
318 <223> OTHER INFORMATION: Modified thymidine
321 <400> SEQUENCE: 21
```
→ not acceptable in an RNA sequence

E--> 322 cuacaucacg ccagucaact t   21
```
325 <210> SEQ ID NO: 22
326 <211> LENGTH: 21
327 <212> TYPE: RNA
328 <213> ORGANISM: Artificial
330 <220> FEATURE:
```

same error as above

```
331 <223> OTHER INFORMATION: Modified thymidine
333 <220> FEATURE:
334 <221> NAME/KEY: modified_base
335 <222> LOCATION: (20)..(20)
336 <223> OTHER INFORMATION: Modified thymidine
```
same
```
339 <400> SEQUENCE: 22
```
E--> 340 guugacuggc gugauguagt t   21
```
343 <210> SEQ ID NO: 23
344 <211> LENGTH: 21
345 <212> TYPE: RNA
```

RAW SEQUENCE LISTING   DATE: 08/28/2006
PATENT APPLICATION: US/10/589,955   TIME: 09:40:09

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\08282006\J589955.raw**

```
        346 <213> ORGANISM: Artificial
        348 <220> FEATURE:
        349 <223> OTHER INFORMATION: Modified thymidine
        351 <220> FEATURE:
        352 <221> NAME/KEY: modified_base
        353 <222> LOCATION: (6)..(6)
        354 <223> OTHER INFORMATION: Modified thymidine
        357 <220> FEATURE:
        358 <221> NAME/KEY: modified_base
        359 <222> LOCATION: (15)..(15)
        360 <223> OTHER INFORMATION: Modified thymidine
        363 <400> SEQUENCE: 23
E--> 364 cuacaucacg ccagucaat t                                       21
        367 <210> SEQ ID NO: 24
        368 <211> LENGTH: 21
        369 <212> TYPE: RNA
        370 <213> ORGANISM: Artificial
        372 <220> FEATURE:
        373 <223> OTHER INFORMATION: Modified thymidine
        375 <220> FEATURE:
        376 <221> NAME/KEY: modified_base
        377 <222> LOCATION: (7)..(7)
        378 <223> OTHER INFORMATION: Modified thymidine
        381 <220> FEATURE:
        382 <221> NAME/KEY: modified_base
        383 <222> LOCATION: (12)..(12)
        384 <223> OTHER INFORMATION: Modified thymidine
        387 <220> FEATURE:
        388 <221> NAME/KEY: modified_base
        389 <222> LOCATION: (15)..(15)
        390 <223> OTHER INFORMATION: Modified thymidine
        393 <220> FEATURE:
        394 <221> NAME/KEY: modified_base
        395 <222> LOCATION: (17)..(17)
        396 <223> OTHER INFORMATION: Modified thymidine
        399 <400> SEQUENCE: 24
E--> 400 guugacuggc gugauguag t t                                      21
        403 <210> SEQ ID NO: 25
        404 <211> LENGTH: 21
        405 <212> TYPE: RNA
        406 <213> ORGANISM: Artificial
        408 <220> FEATURE:
        409 <223> OTHER INFORMATION: Linker
        411 <220> FEATURE:
        412 <221> NAME/KEY: modified_base
        413 <222> LOCATION: (1)..(1)
        414 <223> OTHER INFORMATION: Linker
        417 <220> FEATURE:
        418 <221> NAME/KEY: misc_feature
```

```
                    RAW SEQUENCE LISTING          DATE: 08/28/2006
                    PATENT APPLICATION:  US/10/589,955     TIME: 09:40:09

                        Input Set : A:\PTO.RJ.txt
                        Output Set: N:\CRF4\08282006\J589955.raw

        419 <222> LOCATION: (1)..(1)
        420 <223> OTHER INFORMATION: "n" is -O-CH.sub.2CH.sub.2-O-CH.sub.2CH.sub.2-NH-R.sup.1
        423 <400> SEQUENCE: 25
E-->    424 ncuacaucac gccagucaac tt                                          22
        427 <210> SEQ ID NO: 26
        428 <211> LENGTH: 21
        429 <212> TYPE: RNA
        430 <213> ORGANISM: Artificial
        432 <220> FEATURE:
        433 <223> OTHER INFORMATION: Modified thymidine
        435 <220> FEATURE:
        436 <221> NAME/KEY: modified_base
        437 <222> LOCATION: (20)..(20)
        438 <223> OTHER INFORMATION: Modified thymidine
        441 <400> SEQUENCE: 26
E-->    442 cuacaucacg ccagucaac t                                            21
        445 <210> SEQ ID NO: 27
        446 <211> LENGTH: 22
        447 <212> TYPE: RNA
        448 <213> ORGANISM: Artificial
        450 <220> FEATURE:
        451 <223> OTHER INFORMATION: Modified thymidine
        453 <220> FEATURE:
        454 <221> NAME/KEY: modified_base
        455 <222> LOCATION: (1)..(1)
        456 <223> OTHER INFORMATION: Linker
        459 <220> FEATURE:
        460 <221> NAME/KEY: modified_base
        461 <222> LOCATION: (21)..(21)
        462 <223> OTHER INFORMATION: Modified thymidine
        465 <220> FEATURE:
        466 <221> NAME/KEY: misc_feature
        467 <222> LOCATION: (1)..(1)
        468 <223> OTHER INFORMATION: "n" is -O-CH.sub.2CH.sub.2-O-CH.sub.2CH.sub.2-NH-R.sup.1
        471 <400> SEQUENCE: 27
E-->    472 ncuacaucac gccagucaac tt                                          22
        475 <210> SEQ ID NO: 28
        476 <211> LENGTH: 22
        477 <212> TYPE: RNA
        478 <213> ORGANISM: Artificial
        480 <220> FEATURE:
        481 <223> OTHER INFORMATION: Modified thymidine
        483 <220> FEATURE:
        484 <221> NAME/KEY: modified_base
        485 <222> LOCATION: (1)..(1)
        486 <223> OTHER INFORMATION: Linker
        489 <220> FEATURE:
        490 <221> NAME/KEY: modified_base
        491 <222> LOCATION: (3)..(3)
```

```
492 <223> OTHER INFORMATION: Modified thymidine
495 <220> FEATURE:
496 <221> NAME/KEY: modified_base
497 <222> LOCATION: (7)..(7)
498 <223> OTHER INFORMATION: Modified thymidine
501 <220> FEATURE:
502 <221> NAME/KEY: modified_base
503 <222> LOCATION: (16)..(16)
504 <223> OTHER INFORMATION: Modified thymidine
507 <220> FEATURE:
508 <221> NAME/KEY: modified_base
509 <222> LOCATION: (21)..(21)
510 <223> OTHER INFORMATION: Modified thymidine
513 <220> FEATURE:
514 <221> NAME/KEY: misc_feature
515 <222> LOCATION: (1)..(1)
516 <223> OTHER INFORMATION: "n" is -O-CH.sub.2CH.sub.2-O-CH.sub.2CH.sub.2NH-R.sup.1
519 <400> SEQUENCE: 28
520 ncuacaucac gccagucaac tt                                    22
```

```
<210>   2
<211>   10
<212>   PRT
<213>   PKIfi
<400>   2
```

1) do not <u>not</u> use scientific symbols. They cannot be processed by CRF software.

2) invalid <213> response (see item 10 on Error Summary Sheet)

```
Leu Ala Leu Lys Leu Ala Gly Leu Asp Ile
1               5                   10
```

```
<210>   3
<211>   13
<212>   PRT
<213>   MAPKK
```

same error

↳ This type of error appears in subsequent sequences, too.

7

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:142 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:154 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:280 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:304 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:322 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:340 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:364 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:400 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:424 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:442 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:472 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
L:520 M:321 E: (1) "t" not allowed in RNA Sequence, NUMBER OF INVALID 't' KEYS:2